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RAW SEQUENCE LISTING                    DATE: 04/04/2002
PATENT APPLICATION:  US/09/101,518A     TIME: 15:46:42

        Input Set : A:\PF218US substitute sequence listing.txt
        Output Set: N:\CRF3\04042002\I101518A.raw


    3 <110> APPLICANT: Li, Yi
    5 <120> TITLE OF INVENTION: Human G-Protein Chemokine Receptor HSATU68
    7 <130> FILE REFERENCE: PF218US
    9 <140> CURRENT APPLICATION NUMBER: US 09/101,518A
C--> 10 <141> CURRENT FILING DATE: 2002-03-18
   12 <150> PRIOR APPLICATION NUMBER: PCT/US96/00499
   13 <151> PRIOR FILING DATE: 1996-01-11
   15 <160> NUMBER OF SEQ ID NOS: 9
   17 <170> SOFTWARE: PatentIn version 3.1
   19 <210> SEQ ID NO: 1
   20 <211> LENGTH: 1876
   21 <212> TYPE: DNA
   22 <213> ORGANISM: Homo sapiens
   24 <220> FEATURE:
   25 <221> NAME/KEY: CDS
   26 <222> LOCATION: (173)..(1420)
   27 <223> OTHER INFORMATION:
   30 <400> SEQUENCE: 1
   31 cctgaaggga gagcagggag agagaggaca gtggccagag agggctctgg gcactggagg      60
   33 gacgctcttc ttcctgccca ggggtccctg ggccgatggg atcacgcaga agaatgcgag     120
   35 agaagcagcc tttgagaagg gaagtcacta tcccagagcc cagactgagc gg atg gag     178
   36                                                             Met Glu
   37                                                               1
   39 ttg agg aag tac ggc cct gga aga ctg gcg ggg aca gtt ata gga gga     226
   40 Leu Arg Lys Tyr Gly Pro Gly Arg Leu Ala Gly Thr Val Ile Gly Gly
   41           5                  10                  15
   43 gct gct cag agt aaa tca cag act aaa tca gac tca atc aca aaa gag     274
   44 Ala Ala Gln Ser Lys Ser Gln Thr Lys Ser Asp Ser Ile Thr Lys Glu
   45          20                  25                  30
   47 ttc ctg cca ggc ctt tac aca gcc cct tcc tcc ccg ttc ccg ccc tca     322
   48 Phe Leu Pro Gly Leu Tyr Thr Ala Pro Ser Ser Pro Phe Pro Pro Ser
   49 35                  40                  45                  50
   51 cag gtg agt gac cac caa gtg cta aat gac gcc gag gtt gcc gcc ctc     370
   52 Gln Val Ser Asp His Gln Val Leu Asn Asp Ala Glu Val Ala Ala Leu
   53                  55                  60                  65
   55 ctg gag aac ttc agc tct tcc tat gac tat gga gaa aac gag agt gac     418
   56 Leu Glu Asn Phe Ser Ser Ser Tyr Asp Tyr Gly Glu Asn Glu Ser Asp
   57                  70                  75                  80
   59 tcg tgc tgt acc tcc ccg ccc tgc cca cag gac ttc agc ctg aac ttc     466
   60 Ser Cys Cys Thr Ser Pro Pro Cys Pro Gln Asp Phe Ser Leu Asn Phe
   61          85                  90                  95
   63 gac cgg gcc ttc ctg cca gcc ctc tac agc ctc ctc ttt ctg ctg ggg     514
   64 Asp Arg Ala Phe Leu Pro Ala Leu Tyr Ser Leu Leu Phe Leu Leu Gly
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65      100                     105                     110
67 ctg ctg ggc aac ggc gcg gtg gca gcc gtg ctg ctg agc cgg cgg aca      562
68 Leu Leu Gly Asn Gly Ala Val Ala Ala Val Leu Leu Ser Arg Arg Thr
69 115                     120                     125                     130
71 gcc ctg agc agc acc gac acc ttc ctg ctc cac cta gct gta gca gac      610
72 Ala Leu Ser Ser Thr Asp Thr Phe Leu Leu His Leu Ala Val Ala Asp
73                     135                     140                     145
75 acg ctg ctg gtg ctg aca ctg ccg ctc tgg gca gtg gac gct gcc gtc      658
76 Thr Leu Leu Val Leu Thr Leu Pro Leu Trp Ala Val Asp Ala Ala Val
77                     150                     155                     160
79 cag tgg gtc ttt ggc tct ggc ctc tgc aaa gtg gca ggt gcc ctc ttc      706
80 Gln Trp Val Phe Gly Ser Gly Leu Cys Lys Val Ala Gly Ala Leu Phe
81              165                     170                     175
83 aac atc aac ttc tac gca gga gcc ctc ctg ctg gcc tgc atc agc ttt      754
84 Asn Ile Asn Phe Tyr Ala Gly Ala Leu Leu Leu Ala Cys Ile Ser Phe
85       180                     185                     190
87 gac cgc tac ctg aac ata gtt cat gcc acc cag ctc tac cgc cgg ggg      802
88 Asp Arg Tyr Leu Asn Ile Val His Ala Thr Gln Leu Tyr Arg Arg Gly
89 195                     200                     205                     210
91 ccc ccg gcc cgc gtg acc ctc acc tgc ctg gct gtc tgg ggg ctc tgc      850
92 Pro Pro Ala Arg Val Thr Leu Thr Cys Leu Ala Val Trp Gly Leu Cys
93                     215                     220                     225
95 ctg ctt ttc gcc ctc cca gac ttc atc ttc ctg tcg gcc cac cac gac      898
96 Leu Leu Phe Ala Leu Pro Asp Phe Ile Phe Leu Ser Ala His His Asp
97                     230                     235                     240
99 gag cgc ctc aac gcc acc cac tgc caa tac aac ttc cca cag gtg ggc      946
100 Glu Arg Leu Asn Ala Thr His Cys Gln Tyr Asn Phe Pro Gln Val Gly
101              245                     250                     255
103 cgc acg gct ctg cgg gtg ctg cag ctg gtg gct ggc ttt ctg ctg ccc      994
104 Arg Thr Ala Leu Arg Val Leu Gln Leu Val Ala Gly Phe Leu Leu Pro
105       260                     265                     270
107 ctg ctg gtc atg gcc tac tgc tat gcc cac atc ctg gcc gtg ctg ctg     1042
108 Leu Leu Val Met Ala Tyr Cys Tyr Ala His Ile Leu Ala Val Leu Leu
109 275                     280                     285                     290
111 gtt tcc agg ggc cag cgg cgc ctg cgg gcc atg cgg ctg gtg gtg gtg     1090
112 Val Ser Arg Gly Gln Arg Arg Leu Arg Ala Met Arg Leu Val Val Val
113                     295                     300                     305
115 gtc gtg gtg gcc ttt gcc ctc tgc tgg acc ccc tat cac ctg gtg gtg     1138
116 Val Val Val Ala Phe Ala Leu Cys Trp Thr Pro Tyr His Leu Val Val
117                     310                     315                     320
119 ctg gtg gac atc ctc atg gac ctg ggc gct ttg gcc cgc aac tgt ggc     1186
120 Leu Val Asp Ile Leu Met Asp Leu Gly Ala Leu Ala Arg Asn Cys Gly
121              325                     330                     335
123 cga gaa agc agg gta gac gtg gcc aag tcg gtc acc tca ggc ctg ggc     1234
124 Arg Glu Ser Arg Val Asp Val Ala Lys Ser Val Thr Ser Gly Leu Gly
125       340                     345                     350
127 tac atg cac tgc tgc ctc aac ccg ctg ctc tat gcc ttt gta ggg gtc     1282
128 Tyr Met His Cys Cys Leu Asn Pro Leu Leu Tyr Ala Phe Val Gly Val
129 355                     360                     365                     370
```

```
131 aag ttc cgg gag cgg atg tgg atg ctg ctc ttg cgc ctg ggc tgc ccc      1330
132 Lys Phe Arg Glu Arg Met Trp Met Leu Leu Leu Arg Leu Gly Cys Pro
133             375             380             385
135 aac cag aga ggg ctc cag agg cag cca tcg tct tcc cgc cgg gat tca      1378
136 Asn Gln Arg Gly Leu Gln Arg Gln Pro Ser Ser Ser Arg Arg Asp Ser
137             390             395             400
139 tcc tgg tct gag acc tca gag gcc tcc tac tcg ggc ttg tga          1420
140 Ser Trp Ser Glu Thr Ser Glu Ala Ser Tyr Ser Gly Leu
141             405             410             415
143 ggccggaatc cgggctcccc tttcgcccac agtctgactt ccccgcattc caggctcctc   1480
145 cctccctctg ccggctctgg ctctccccaa tatcctcgct cccgggactc actggcagcc   1540
147 ccagcaccac caggtctccc gggaagccac cctcccagct ctgaggactg caccattgct   1600
149 gctccttagc tgccaagccc catcctgccg cccgaggtgg ctgcctggag ccccactgcc   1660
151 cttctcattt ggaaactaaa acttcatctt ccccaagtgc ggggagtaca aggcatggcg   1720
153 tagagggtgc tgccccatga agccacagcc caggcctcca gctcagcagt gactgtggcc   1780
155 atggtcccca agacctctat atttggtctt ttattttat gtctaaaatc ctgcttaaaa    1840
157 cttttcaata aacaagatcg tcaggaaaaa aaaaaa                            1876
160 <210> SEQ ID NO: 2
161 <211> LENGTH: 415
162 <212> TYPE: PRT
163 <213> ORGANISM: Homo sapiens
165 <400> SEQUENCE: 2
167 Met Glu Leu Arg Lys Tyr Gly Pro Gly Arg Leu Ala Gly Thr Val Ile
168 1               5                   10                  15
171 Gly Gly Ala Ala Gln Ser Lys Ser Gln Thr Lys Ser Asp Ser Ile Thr
172             20                  25                  30
175 Lys Glu Phe Leu Pro Gly Leu Tyr Thr Ala Pro Ser Ser Pro Phe Pro
176             35                  40                  45
179 Pro Ser Gln Val Ser Asp His Gln Val Leu Asn Asp Ala Glu Val Ala
180         50                  55                  60
183 Ala Leu Leu Glu Asn Phe Ser Ser Ser Tyr Asp Tyr Gly Glu Asn Glu
184 65                  70                  75                  80
187 Ser Asp Ser Cys Cys Thr Ser Pro Pro Cys Pro Gln Asp Phe Ser Leu
188             85                  90                  95
191 Asn Phe Asp Arg Ala Phe Leu Pro Ala Leu Tyr Ser Leu Leu Phe Leu
192             100             105             110
195 Leu Gly Leu Leu Gly Asn Gly Ala Val Ala Ala Val Leu Leu Ser Arg
196         115             120             125
199 Arg Thr Ala Leu Ser Ser Thr Asp Thr Phe Leu Leu His Leu Ala Val
200         130             135             140
203 Ala Asp Thr Leu Leu Val Leu Thr Leu Pro Leu Trp Ala Val Asp Ala
204 145             150             155             160
207 Ala Val Gln Trp Val Phe Gly Ser Gly Leu Cys Lys Val Ala Gly Ala
208             165             170             175
211 Leu Phe Asn Ile Asn Phe Tyr Ala Gly Ala Leu Leu Leu Ala Cys Ile
212             180             185             190
215 Ser Phe Asp Arg Tyr Leu Asn Ile Val His Ala Thr Gln Leu Tyr Arg
216         195             200             205
219 Arg Gly Pro Pro Ala Arg Val Thr Leu Thr Cys Leu Ala Val Trp Gly
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```
220      210                    215                    220
223 Leu Cys Leu Leu Phe Ala Leu Pro Asp Phe Ile Phe Leu Ser Ala His
224 225                    230                    235                    240
227 His Asp Glu Arg Leu Asn Ala Thr His Cys Gln Tyr Asn Phe Pro Gln
228                    245                    250                    255
231 Val Gly Arg Thr Ala Leu Arg Val Leu Gln Leu Val Ala Gly Phe Leu
232                    260                    265                    270
235 Leu Pro Leu Leu Val Met Ala Tyr Cys Tyr Ala His Ile Leu Ala Val
236               275                    280                    285
239 Leu Leu Val Ser Arg Gly Gln Arg Arg Leu Arg Ala Met Arg Leu Val
240      290                    295                    300
243 Val Val Val Val Val Ala Phe Ala Leu Cys Trp Thr Pro Tyr His Leu
244 305                    310                    315                    320
247 Val Val Leu Val Asp Ile Leu Met Asp Leu Gly Ala Leu Ala Arg Asn
248                    325                    330                    335
251 Cys Gly Arg Glu Ser Arg Val Asp Val Ala Lys Ser Val Thr Ser Gly
252               340                    345                    350
255 Leu Gly Tyr Met His Cys Cys Leu Asn Pro Leu Leu Tyr Ala Phe Val
256               355                    360                    365
259 Gly Val Lys Phe Arg Glu Arg Met Trp Met Leu Leu Leu Arg Leu Gly
260      370                    375                    380
263 Cys Pro Asn Gln Arg Gly Leu Gln Arg Gln Pro Ser Ser Ser Arg Arg
264 385                    390                    395                    400
267 Asp Ser Ser Trp Ser Glu Thr Ser Glu Ala Ser Tyr Ser Gly Leu
268               405                    410                    415
271 <210> SEQ ID NO: 3
272 <211> LENGTH: 29
273 <212> TYPE: DNA
274 <213> ORGANISM: Artificial sequence
276 <220> FEATURE:
277 <223> OTHER INFORMATION: Contains a BamHI restriction enzyme site
279 <400> SEQUENCE: 3
280 cgggatcctc catggagttg aggaagtac                                    29
283 <210> SEQ ID NO: 4
284 <211> LENGTH: 30
285 <212> TYPE: DNA
286 <213> ORGANISM: Artificial sequence
288 <220> FEATURE:
289 <223> OTHER INFORMATION: Contains complementary sequences to a BamHI site
291 <400> SEQUENCE: 4
292 ggcggatccc gctcacaagc ccgagtagga                                    30
295 <210> SEQ ID NO: 5
296 <211> LENGTH: 34
297 <212> TYPE: DNA
298 <213> ORGANISM: Artificial sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: Contains a HindIII site
303 <400> SEQUENCE: 5
304 gtccaagctt gccaccatgg agttgaggaa gtac                              34
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        Input Set : A:\PF218US substitute sequence listing.txt
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307 <210> SEQ ID NO: 6
308 <211> LENGTH: 57
309 <212> TYPE: DNA
310 <213> ORGANISM: Artificial sequence
312 <220> FEATURE:
313 <223> OTHER INFORMATION: Contains complementary sequences to a XhoI site, translation
stop
314       codon, and an HA tag
316 <400> SEQUENCE: 6
317 ctgctcgagt caagcgtagt ctgggacgtc gtatgggtag cacaagcccg agtagga          57
320 <210> SEQ ID NO: 7
321 <211> LENGTH: 31
322 <212> TYPE: DNA
323 <213> ORGANISM: Artificial sequence
325 <220> FEATURE:
326 <223> OTHER INFORMATION: Contains a BamHI restriction enzyme site followed by 5
nucleotide
327       s resembling an efficient signal for the initiation of translatio
328       n in eukaryotic cells (J. Mol. Biol. 1987, 196, 947-950, Kozak, M
329       .)
331 <400> SEQUENCE: 7
332 cgggatccct cccatggagt tgaggaagta c                                     31
335 <210> SEQ ID NO: 8
336 <211> LENGTH: 29
337 <212> TYPE: DNA
338 <213> ORGANISM: Artificial sequence
340 <220> FEATURE:
341 <223> OTHER INFORMATION: Contains the cleavage site for the restriction endonuclease
BamHI
343 <400> SEQUENCE: 8
344 cgggatcccg ctcacaagcc cgagtagga                                        29
347 <210> SEQ ID NO: 9
348 <211> LENGTH: 353
349 <212> TYPE: PRT
350 <213> ORGANISM: Homo sapiens
352 <400> SEQUENCE: 9
354 Glu Ser Asp Ser Phe Glu Asp Phe Trp Lys Gly Glu Asp Leu Ser Asn
355 1               5                   10                  15
358 Tyr Ser Tyr Ser Ser Thr Leu Pro Pro Phe Leu Leu Asp Ala Ala Pro
359             20                  25                  30
362 Cys Glu Pro Glu Ser Leu Glu Ile Asn Lys Tyr Phe Val Val Ile Ile
363         35                  40                  45
366 Tyr Ala Leu Val Phe Leu Leu Ser Leu Leu Gly Asn Ser Leu Val Met
367     50                  55                  60
370 Leu Val Ile Leu Tyr Ser Arg Val Gly Arg Ser Val Thr Asp Val Tyr
371 65                  70                  75                  80
374 Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu Thr Leu Pro
375             85                  90                  95
378 Ile Trp Ala Ala Ser Lys Val Asn Gly Trp Ile Phe Gly Thr Phe Leu
379             100                 105                 110
382 Cys Lys Val Val Ser Leu Leu Lys Glu Val Asn Phe Tyr Ser Gly Ile
383         115                 120                 125
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VERIFICATION SUMMARY   DATE: 04/04/2002
PATENT APPLICATION: US/09/101,518A   TIME: 15:46:43

Input Set : **A:\PF218US substitute sequence listing.txt**
Output Set: **N:\CRF3\04042002\I101518A.raw**

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date